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GTC ACA GCA TAT AAA GAG GGA TAT GGA GAG GGC TGC GTA ACG ATC CAT 3168
Val Thr Ala Tyr Lys Glu Gly Tyr Gly Glu Gly Cys Val Thr Ile His
1045 1050 1055

5 GAG ATC GAA GAC AAT ACA GAC GAA CTG AAA TTC AGC AAC TGT GTA GAA 3216
Glu Ile Glu Asp Asn Thr Asp Glu Leu Lys Phe Ser Asn Cys Val Glu
1060 1065 1070

10 GAG GAA GTA TAT CCA AAC AAC ACA GTA ACG TGT AAT AAT TAT ACT GGG 3264
Glu Glu Val Tyr Pro Asn Asn Thr Val Thr Cys Asn Asn Tyr Thr Gly
1075 1080 1085

15 ACT CAA GAA GAA TAT GAG GGT ACG TAC ACT TCT CGT AAT CAA GGA TAT 3312
Thr Gln Glu Glu Tyr Glu Gly Thr Tyr Thr Ser Arg Asn Gln Gly Tyr
1090 1095 1100

GAC GAA GCC TAT GGT AAT AAC CCT TCC GTA CCA GCT GAT TAC GCT TCA 3360
Asp Glu Ala Tyr Gly Asn Asn Pro Ser Val Pro Ala Asp Tyr Ala Ser
1105 1110 1115 1120

GTC TAT GAA GAA AAA TCG TAT ACA GAT GGA CGA AGA GAG AAT CCT TGT 3408
Val Tyr Glu Glu Lys Ser Tyr Thr Asp Gly Arg Arg Glu Asn Pro Cys
1125 1130 1135

25 GAA TCT AAC AGA GGC TAT GGG GAT TAC ACA CCA CTA CCG GCT GGT TAT 3456
Glu Ser Asn Arg Gly Tyr Gly Asp Tyr Thr Pro Leu Pro Ala Gly Tyr
1140 1145 1150

30 GTA ACA AAG GAT TTA GAG TAC TTC CCA GAG ACC GAT AAG GTA TGG ATT 3504
Val Thr Lys Asp Leu Glu Tyr Phe Pro Glu Thr Asp Lys Val Trp Ile
1155 1160 1165

35 GAG ATC GGA GAA ACA GAA GGA ACA TTC ATC GTG GAT AGC GTG GAA TTA 3552
Glu Ile Gly Glu Thr Glu Gly Thr Phe Ile Val Asp Ser Val Glu Leu
1170 1175 1180

40 CTC CTT ATG GAG GAA 3567
Leu Leu Met Glu Glu
1185

(2) INFORMATION FOR SEQ ID NO:6:

45 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1189 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

50 (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Glu Glu Asn Asn Gln Asn Gln Cys Ile Pro Tyr Asn Cys Leu Ser
1 5 10 15

	Asn	Pro	Glu	Glu	Val	Leu	Leu	Asp	Gly	Glu	Arg	Ile	Ser	Thr	Gly	Asn	
				20					25						30		
5	Ser	Ser	Ile	Asp	Ile	Ser	Leu	Ser	Leu	Val	Gln	Phe	Leu	Val	Ser	Asn	
			35					40					45				
	Phe	Val	Pro	Gly	Gly	Gly	Phe	Leu	Val	Gly	Leu	Ile	Asp	Phe	Val	Trp	
		50					55					60					
10	Gly	Ile	Val	Gly	Pro	Ser	Gln	Trp	Asp	Ala	Phe	Leu	Val	Gln	Ile	Glu	
	65					70					75					80	
	Gln	Leu	Ile	Asn	Glu	Arg	Ile	Ala	Glu	Phe	Ala	Arg	Asn	Ala	Ala	Ile	
15					85				90						95		
	Ala	Asn	Leu	Glu	Gly	Leu	Gly	Asn	Asn	Phe	Asn	Ile	Tyr	Val	Glu	Ala	
				100				105						110			
20	Phe	Lys	Glu	Trp	Glu	Glu	Asp	Pro	Asn	Asn	Pro	Ala	Thr	Arg	Thr	Arg	
			115					120						125			
	Val	Ile	Asp	Arg	Phe	Arg	Ile	Leu	Asp	Gly	Leu	Leu	Glu	Arg	Asp	Ile	
		130					135					140					
25	Pro	Ser	Phe	Arg	Ile	Ser	Gly	Phe	Glu	Val	Pro	Leu	Leu	Ser	Val	Tyr	
	145					150					155				160		
	Ala	Gln	Ala	Ala	Asn	Leu	His	Leu	Ala	Ile	Leu	Arg	Asp	Ser	Val	Ile	
					165					170					175		
	Phe	Gly	Glu	Ala	Trp	Gly	Leu	Thr	Thr	Ile	Asn	Val	Asn	Glu	Asn	Tyr	
			180						185					190			
35	Asn	Arg	Leu	Ile	Arg	His	Ile	Asp	Glu	Tyr	Ala	Asp	His	Cys	Ala	Asn	
		195						200					205				
	Thr	Tyr	Asn	Arg	Gly	Leu	Asn	Asn	Leu	Pro	Lys	Ser	Thr	Tyr	Gln	Asp	
		210					215						220				
40	Trp	Ile	Thr	Tyr	Asn	Arg	Leu	Arg	Arg	Asp	Leu	Thr	Leu	Thr	Val	Leu	
	225					230					235				240		
	Asp	Ile	Ala	Ala	Phe	Phe	Pro	Asn	Tyr	Asp	Asn	Arg	Arg	Tyr	Pro	Ile	
45					245					250					255		
	Gln	Pro	Val	Gly	Gln	Leu	Thr	Arg	Glu	Val	Tyr	Thr	Asp	Pro	Leu	Ile	
				260					265					270			
50	Asn	Phe	Asn	Pro	Gln	Leu	Gln	Ser	Val	Ala	Gln	Leu	Pro	Thr	Phe	Asn	
		275						280					285				
	Val	Met	Glu	Ser	Ser	Ala	Ile	Arg	Asn	Pro	His	Leu	Phe	Asp	Ile	Leu	
		290					295					300					

	Asn	Asn	Leu	Thr	Ile	Phe	Thr	Asp	Trp	Phe	Ser	Val	Gly	Arg	Asn	Phe	
	305					310					315					320	
5	Tyr	Trp	Gly	Gly	His	Arg	Val	Ile	Ser	Ser	Leu	Ile	Gly	Gly	Gly	Asn	
					325					330					335		
	Ile	Thr	Ser	Pro	Ile	Tyr	Gly	Arg	Glu	Ala	Asn	Gln	Glu	Pro	Pro	Arg	
				340					345					350			
10	Ser	Phe	Thr	Phe	Asn	Gly	Pro	Val	Phe	Arg	Thr	Leu	Ser	Asn	Pro	Thr	
			355					360					365				
	Leu	Arg	Leu	Leu	Gln	Gln	Pro	Trp	Pro	Ala	Pro	Pro	Phe	Asn	Leu	Arg	
15		370					375					380					
	Gly	Val	Glu	Gly	Val	Glu	Phe	Ser	Thr	Pro	Thr	Asn	Ser	Phe	Thr	Tyr	
	385					390					395					400	
20	Arg	Gly	Arg	Gly	Thr	Val	Asp	Ser	Leu	Thr	Glu	Leu	Pro	Pro	Glu	Asp	
					405					410					415		
	Asn	Ser	Val	Pro	Pro	Arg	Glu	Gly	Tyr	Ser	His	Arg	Leu	Cys	His	Ala	
				420					425					430			
25	Thr	Phe	Val	Gln	Arg	Ser	Gly	Thr	Pro	Phe	Leu	Thr	Thr	Gly	Val	Val	
			435					440					445				
	Phe	Ser	Trp	Thr	His	Arg	Ser	Ala	Thr	Leu	Thr	Asn	Thr	Ile	Asp	Pro	
		450					455					460					
	Glu	Arg	Ile	Asn	Gln	Ile	Pro	Leu	Val	Lys	Gly	Phe	Arg	Val	Trp	Gly	
	465					470				475						480	
35	Gly	Thr	Ser	Val	Ile	Thr	Gly	Pro	Gly	Phe	Thr	Gly	Gly	Asp	Ile	Leu	
					485				490						495		
	Arg	Arg	Asn	Thr	Phe	Gly	Asp	Phe	Val	Ser	Leu	Gln	Val	Asn	Ile	Asn	
			500						505					510			
40	Ser	Pro	Ile	Thr	Gln	Arg	Tyr	Arg	Leu	Arg	Phe	Arg	Tyr	Ala	Ser	Ser	
			515					520					525				
	Arg	Asp	Ala	Arg	Val	Ile	Val	Leu	Thr	Gly	Ala	Ala	Ser	Thr	Gly	Val	
45		530					535				540						
	Gly	Gly	Gln	Val	Ser	Val	Asn	Met	Pro	Leu	Gln	Lys	Thr	Met	Glu	Ile	
	545					550					555					560	
50	Gly	Glu	Asn	Leu	Thr	Ser	Arg	Thr	Phe	Arg	Tyr	Thr	Asp	Phe	Ser	Asn	
					565				570					575			
	Pro	Phe	Ser	Phe	Arg	Ala	Asn	Pro	Asp	Ile	Ile	Gly	Ile	Ser	Glu	Gln	
				580				585						590			